

# 10086816 Results

SEQ ID NO: 2

## SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	2849	100.0	550	21	AAY44278	Human organic anion transporter; Homo sapiens.
2	2849	100.0	550	22	AAB47271	HOAT1. Homo sapiens.
3	2832.5	99.4	563	20	AAW88489	Human organic anion transporter; Homo sapiens.
4	2538.5	89.1	551	20	AAW88488	Rat organic anion transporter; Rat.
5	2463.5	86.5	545	22	AAB36553	Mouse organic anion transporter; Mouse.
6	1416	49.7	542	22	AAB47274	HOAT3. Homo sapiens.
7	1415	49.7	542	21	AAY92902	Human cerebral organic anion transporter; Homo sapiens.
8	1373.5	48.2	561	18	AAW44196	Human osteoclast transporter; Human.
9	1371	48.1	537	18	AAW44195	Mouse osteoclast transporter; Mouse.
10	1370	48.1	536	21	AAY92903	Rat cerebral organic anion transporter; Rat.
11	1287.5	45.2	557	24	ABU54646	Human NOVX polypeptide; Human.
12	1266.5	44.5	556	24	ABJ37918	NOVX protein sequence; Human.
13	1264	44.4	584	23	ABP70090	Human NOV18a. Homologous protein; Human.
14	1250	43.9	589	23	AAE13280	Human transporters; Human.
15	1249.5	43.9	573	24	ABJ37917	NOVX protein sequence; Human.
16	1231	43.2	778	24	ABP54440	Human TCH110 protein; Human.
17	1227.5	43.1	553	22	AAE10332	Human transporter; Human.
18	1227.5	43.1	553	23	ABP70091	Human NOV19a. Homologous protein; Human.
19	1211.5	42.5	815	22	ABG26899	Novel human diaphragm protein; Human.
20	1208	42.4	578	22	AAE06571	Human protein having homology with NOVX; Human.
21	1173.5	41.2	553	24	ABG73329	Human organic ion transporter; Human.
22	1133	39.8	550	22	AAE06612	Human protein having homology with NOVX; Human.
23	1133	39.8	550	22	AAB69091	Human organic anion transporter; Human.
24	1133	39.8	550	23	AAE16772	Human transporter; Human.
25	1133	39.8	550	24	ABB82969	Human SLC22A relative; Human.

### RESULT 1

AAY44278

ID AAY44278 standard; Protein; 550 AA.

XX

AC AAY44278;

XX

DT 29-FEB-2000 (first entry)

XX

DE Human organic anion transporter.

XX

KW Human organic anion transporter; HOAT; nephrotoxic compound; screen; drug-drug interaction; nucleotide phosphonate.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 515..528

FT /label= Immunogen

FT /note= "For producing antibodies"

XX

PN WO9964459-A2.

XX

PD 16-DEC-1999.

XX

PF 10-JUN-1999; 99WO-US13172.

XX

PR 11-JUN-1998; 98US-0088864.

PR 03-MAY-1999; 99US-0132267.

XX

PA (GILE-) GILEAD SCI INC.

XX

PI Cihlar T;

XX

DR WPI; 2000-097519/08.

DR N-PSDB; AAZ29300.  
 XX  
 PT Human organic anion transporter nucleic acid used in drug screening,  
 PT identifying drug-drug interactions or individuals in whom particular  
 PT drugs are nephrotoxic -  
 XX  
 PS Claim 9; Fig 1; 36pp; English.  
 XX  
 CC The present sequence is human organic anion transporter (hOAT) protein.  
 CC hOAT is expressed in kidney and brain and removes toxic anions  
 CC from the circulation. It can be produced in host cells by transforming  
 CC them with recombinant vectors containing nucleic acid encoding hOAT.  
 CC It can be used in screening for compounds that suppress or enhance anion  
 CC uptake and transport by hOAT, to identify molecular variants of  
 CC nephrotoxic compounds, to detect drug-drug interaction within kidney  
 CC and brain and to test for transport of a covalently modified form of a  
 CC nucleotide phosphonate analogue by hOAT.  
 XX  
 SQ Sequence 550 AA;

Query Match 100.0%; Score 2849; DB 21; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-281;  
 Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLMASHNTLQNFTAAIPTHCRPPADANLSKN 60
Db	1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLMASHNTLQNFTAAIPTHCRPPADANLSKN 60
Qy	61 GGLEVWLPRDRQGPESCLRFSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120
Db	61 GGLEVWLPRDRQGPESCLRFSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120
Qy	121 VTEWDLVCNSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA 180
Db	121 VTEWDLVCNSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA 180
Qy	181 FAPNFPIYCAFRLLSGMALAGISLNCTLNVEWMPITHRACVGTLIGYVYSLGQFLLAGV 240
Db	181 FAPNFPIYCAFRLLSGMALAGISLNCTLNVEWMPITHRACVGTLIGYVYSLGQFLLAGV 240
Qy	241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300
Db	241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300
Qy	301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRLFLCLSMWFATSFAYYGLVMDL 360
Db	301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRLFLCLSMWFATSFAYYGLVMDL 360
Qy	361 QGFGVSIYLIQVIFGAVDLPALKVGFVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420
Db	361 QGFGVSIYLIQVIFGAVDLPALKVGFVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420
Qy	421 IVRTSLAVLGKGCLAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
Db	421 IVRTSLAVLGKGCLAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
Qy	481 LYPSMPLFIYGVPAVAASAVTVLLPETLGQPLPDTVQDLESRKQTRQQQEHQKYMVPL 540
Db	481 LYPSMPLFIYGVPAVAASAVTVLLPETLGQPLPDTVQDLESRKQTRQQQEHQKYMVPL 540
Qy	541 QASAQEKNGL 550
Db	541 QASAQEKNGL 550

RESULT 2  
 AAB47271  
 ID AAB47271 standard; Protein; 550 AA.  
 XX  
 AC AAB47271;  
 XX

DT 06-AUG-2001 (first entry)  
XX  
DE hOAT1.  
XX  
KW Human; organic anion transporter; hOAT; liver; kidney;  
KW membrane protein; transport; organic anion; splice variant.  
XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT Modified-site 271  
FT /note= "PKC phosphorylation site"  
FT Modified-site 278  
FT /note= "PKC phosphorylation site"  
FT Modified-site 284  
FT /note= "PKC phosphorylation site"  
XX

PN WO200104283-A2.

XX  
PD 18-JAN-2001.

XX  
PF 12-JUL-2000; 2000WO-US18980.

XX  
PR 12-JUL-1999; 99US-0143771.

XX  
PA (META-) METABASIS THERAPEUTICS INC.  
XX

PI Sun W;

XX  
DR WPI; 2001-367057/38.

DR N-PSDB; AAC85819.

XX  
PT Nucleic acids encoding human organic anion transporter polypeptides,  
PT useful in gene therapy procedures -

XX  
PS Example 2; Fig 1; 95pp; English.

XX  
CC The sequences given in AAB47271-76 represent human organic anion  
CC transporter (hOAT) polypeptides. hOAT polypeptides are preferentially  
CC expressed in the liver and kidneys of humans. OAT's are membrane  
CC proteins that facilitate the transport of organic anions across the  
CC cell membrane. The mechanism of transport is thought to be a secondary  
CC or tertiary active transport involving exchange of another organic anion.  
CC hOAT2A and hOAT2B are thought to be splice variants as they are  
CC identical except at the C-terminal end. hOAT proteins and the DNA  
CC encoding them, may be used in the prevention, treatment and diagnosis  
CC of diseases associated with inappropriate hOAT expression.

XX  
SQ Sequence 550 AA;

Query Match 100.0%; Score 2849; DB 22; Length 550;  
Best Local Similarity 100.0%; Pred. No. 2.6e-281;  
Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMAHNTLQNFTAAIPTHCRPPADANLSKN 60  
Db 1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMAHNTLQNFTAAIPTHCRPPADANLSKN 60

Qy 61 GGLEVWLPRDRQGPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120  
Db 61 GGLEVWLPRDRQGPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120

Qy 121 VTEWDLVCSHRALRQLAQSLYMGVVLGAMVFGYLADRLGRRKVLILNYLQTAVGTC 180  
Db 121 VTEWDLVCSHRALRQLAQSLYMGVVLGAMVFGYLADRLGRRKVLILNYLQTAVGTC 180

Qy 181 FAPNFPPIYCAFRLLSGMALAGISLNCTLNVEWMPITHTRACVGTLLIGYVYSLGQFLLAGV 240  
Db 181 FAPNFPPIYCAFRLLSGMALAGISLNCTLNVEWMPITHTRACVGTLLIGYVYSLGQFLLAGV 240

Qy 241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300

Db ||||||| 241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300  
Qy 301 GAKLSMEVLRASLQKELETMGKQASAMELLRCPTLRHFLCLSLMLWFATSFAYYGLVMDL 360  
Db ||||||| 301 GAKLSMEVLRASLQKELETMGKQASAMELLRCPTLRHFLCLSLMLWFATSFAYYGLVMDL 360  
Qy 361 QGFGVSIYLIQVIFGAVIDLPAKLVLGFLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420  
Db ||||||| 361 QGFGVSIYLIQVIFGAVIDLPAKLVLGFLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420  
Qy 421 IVRTSLAVLGKGCLAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480  
Db ||||||| 421 IVRTSLAVLGKGCLAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480  
Qy 481 LYPSMPLFIYGAAPVAASAVTVLLPETLGQPLPDTVQDLESRKGKQTRQQQEHQKYMVPL 540  
Db ||||||| 481 LYPSMPLFIYGAAPVAASAVTVLLPETLGQPLPDTVQDLESRKGKQTRQQQEHQKYMVPL 540  
Qy 541 QASAQEKNGL 550  
Db ||||||| 541 QASAQEKNGL 550

RESULT 3

AAW88489

ID AAW88489 standard; Protein; 563 AA.

XX

AC AAW88489;

XX

DT 05-MAR-1999 (first entry)

XX

DE Human organic anion transporter OAT-1.

XX

KW Organic anion transporter; OAT-1; nephrotoxicity; drug release;

KW drug-drug interaction mechanism; drug elimination; kidney;

KW beta-lactam antibiotic; non-steroidal antiinflammatory; diuretic.

XX

OS Homo sapiens.

XX

PN WO9853064-A1.

XX

PD 26-NOV-1998.

XX

PF 18-MAY-1998; 98WO-JP02171.

XX

PR 23-MAY-1997; 97JP-0134182.

XX

PA (TANA ) TANABE SEIYAKU CO.

XX

PI Endou H, Hosoyamada M, Kanai Y, Sekine T;

XX

DR WPI; 1999-045310/04.

DR N-PSDB; AAV79585.

XX

PT New renal organic anion transporter protein - useful for, e.g.

PT screening potential drugs for prevention of nephrotoxicity and as a

PT reagent for the investigation of drug metabolism

XX

PS Claim 1; Page 27-32; 45pp; Japanese.

XX

CC The present sequence represents human organic anion transporter protein

CC OAT-1. OAT-1 may be used as a reagent for the in vitro analysis and

CC study of drug release and drug-drug interaction mechanisms and drug

CC elimination via the kidney (e.g. for drugs such as beta-lactam

CC antibiotics, non-steroidal antiinflammatories and diuretics), and as

CC a reagent for screening candidate drugs for the prevention of

CC nephrotoxicity. Oligonucleotide sequences which hybridise to the OAT-1

CC polynucleotide may be used as probes for detection of OAT-1 gene

CC sequences.

XX

SQ Sequence 563 AA;

Query Match 99.4%; Score 2832.5; DB 20; Length 563;  
Best Local Similarity 97.7%; Pred. No. 1.3e-279;  
Matches 550; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHCRPPADANLSKN 60  
Db 1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHCRPPADANLSKN 60

Qy 61 GGLEVWLPRDRQGPESCLRFSTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120  
Db 61 GGLEVWLPRDRQGPESCLRFSTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120

Qy 121 VTEWDLVCNSHRLRQLAQSLYMGVLLGAMVFGYLADRIGRRKVLILNYLQTAVSGTCAA 180  
Db 121 VTEWDLVCNSHRLRQLAQSLYMGVLLGAMVFGYLADRIGRRKVLILNYLQTAVSGTCAA 180

Qy 181 FAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTLIGYVYSLGQFLLAGV 240  
Db 181 FAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTLIGYVYSLGQFLLAGV 240

Qy 241 AYAVPHWRHLQLLVSAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300  
Db 241 AYAVPHWRHLQLLVSAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300

Qy 301 GAKLMSMEVLRASLQKELTMGKGQASAMELLRCPTLRLFLCLSMWFATSFAYYGLVMDL 360  
Db 301 GAKLMSMEVLRASLQKELTMGKGQASAMELLRCPTLRLFLCLSMWFATSFAYYGLVMDL 360

Qy 361 QGFGVSIYLIQVIFGAVDLPKAFLVGLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420  
Db 361 QGFGVSIYLIQVIFGAVDLPKAFLVGLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420

Qy 421 IVRTSLAVLGKGCLAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480  
Db 421 IVRTSLAVLGKGCLAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480

Qy 481 LYPSMPLFIYGAAPVAASAVTVLLPETLGQPLPDTVQDLES-----RKGKQT 527  
Db 481 LYPSMPLFIYGAAPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT 540

Qy 528 RQQQEHQKYMVPLQASAQEKNGL 550  
Db 541 RQQQEHQKYMVPLQASAQEKNGL 563

Issued:

SUMMARIES

%						
Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2849	100.0	550	4	US-09-330-245A-2	Sequence 2, Appli
2	2463.5	86.5	545	4	US-09-572-147-2	Sequence 2, Appli
3	1371	48.1	537	2	US-08-647-397-2	Sequence 2, Appli
4	704	24.7	556	3	US-08-501-572-1	Sequence 1, Appli
5	704	24.7	556	3	US-09-040-444-1	Sequence 1, Appli
6	699.5	24.6	555	3	US-08-501-572-3	Sequence 3, Appli
7	699.5	24.6	555	3	US-09-040-444-3	Sequence 3, Appli
8	674	23.7	553	3	US-08-501-572-2	Sequence 2, Appli
9	674	23.7	553	3	US-09-040-444-2	Sequence 2, Appli

RESULT 2

US-09-572-147-2

; Sequence 2, Application US/09572147

; Patent No. 6420544  
; GENERAL INFORMATION:  
; APPLICANT: Lin Yue  
; APPLICANT: John Feild  
; APPLICANT: Harma Ellens  
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES  
; TITLE OF INVENTION: ENCODING MURINE ORGANIC ANION TRANSPORTER 5 (mOATP5) AND  
; TITLE OF INVENTION: SCREENING METHODS THEREOF  
; FILE REFERENCE: GP-70622  
; CURRENT APPLICATION NUMBER: US/09/572,147  
; CURRENT FILING DATE: 2000-05-17  
; PRIOR APPLICATION NUMBER: 60/134,879  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 545  
; TYPE: PRT  
; ORGANISM: MUS MUSCULUS  
US-09-572-147-2

Query Match 86.5%; Score 2463.5; DB 4; Length 545;  
 Best Local Similarity 85.1%; Pred. No. 8.9e-251;  
 Matches 469; Conservative 41; Mismatches 34; Indels 7; Gaps 2;

Qy 1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHICRPPADANLSKN 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 1 MAFNDLLKQVGGVGRFQLIQVTMVVAPLLLMAHNTLQNFTAAIPAHICRPPANANLSKD 60

Qy 61 GGLEVWLPRDRQGPESCLRFTEPWQGLPFLNGTEANGTGATEPCTDGWYIDNSTFPSTI 120  
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 61 GGLEAWLPLDKQGRPESCLRFPFPH-----NGTEANGTGVTETPCLDGWYIDNSTFPSTI 114

Qy 121 VTEWDLVCSSHRAIRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAWSGTCAA 180  
 |||||:|||||:|||||:|||||:|||||:  
 Db 115 VTEWNLVCSSHRAFRQLAQSLFMVGVLLGAMMFGYLADRLGRRKVLILNYLQTAWSGTCAA 174

Qy 181 FAPNFPIYCAFRLLSGMALAGISLNCTLNVEWMPIHTRACVGTLIGVYVSLGQFLLAGV 240  
 :|||: :|||: :|||: :|||: :|||: :|||:  
 Db 175 YAPNVTYVICFRLLSGMSLASIAINCMTLNMEWMPIHTRAYVGTLIGVYVSLGQFLLAGI 234

Qy 241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSGRLDLTLRALQRVARINGKREE 300  
 |||||:|||:|||:|||:|||:|||:|||:  
 Db 235 AYAVPHWRHLQLAVSVPPFFVAFIYSWFFIESARWYSSGRLDLTLRALQRVARINGKQEE 294

Qy 301 GAKLSMEVLRASLQKELTMKGQASAMELLRCPTLRLFLCLSMMLWFATSFAYYGLVMDL 360  
 |||||:|||:|||:|||:|||:|||:|||:  
 Db 295 GAKLSIEVLQTSLQKELTLNKQASAMELLRCPTLRRFLCLSMMLWFATSFAYYGLVMDL 354

Qy 361 QGFGVSIYLIQVIFGAVDLPKAFLVGLFLVINSLGRRPAQMAALLLAGICILLNGVIHQDQS 420  
 |||||:|||:|||:|||:|||:|||:|||:  
 Db 355 QGFGVSMYLIQVIFGAVDLPKAFLVCFLVINSMGRRPAQLASLLLAGICILVNGIIPRGHT 414

Qy 421 IVRTSLAVLGKGCLAASFNCIFLYTGEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480  
 :|||:|||:|||:|||:|||:|||:|||:  
 Db 415 IIRTSLSAVLGKGCLASSFNCIFLYTGEYPTMIRQTGLGMGSTMARVGSIVSPLISMATAE 474

Qy 481 LYPSMPLFIYGAHPVAASAVTLLPETLGQPLPDTVQDLESR-KKGKQTRQQQEHQKYMVP 539  
 |||||:|||:|||:|||:|||:|||:  
 Db 475 FYPSPILFIFGAVPVAASAVTALLPETLGQPLPDTVQDLSRSRGKQKQQQLEQQKQMIP 534

Qy 540 LQASAQEKNGL 550  
 |||:|||:  
 Db 535 LQVSTQEKNGL 545

## SUMMARIES

Result	Score	% Query				Description
		Match	Length	DB	ID	

1	723	25.4	593	2	JC4884	organic cation tra
2	709	24.9	556	2	S50862	organic cation tra
3	644.5	22.6	576	2	T22509	hypothetical prote
4	641	22.5	557	2	JW0089	organic cation tra
5	617.5	21.7	557	2	JE0346	high-affinity carn
6	450.5	15.8	794	2	T27870	hypothetical prote
7	450	15.8	745	2	T16565	hypothetical prote
8	434.5	15.3	539	2	C96758	probable protein
9	408.5	14.3	515	2	B96825	hypothetical prote
10	401.5	14.1	527	2	T01019	transport protein
11	395.5	13.9	447	2	D89646	protein ZK455.8 [i]
12	391	13.7	521	2	H86298	hypothetical prote

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	734.5	25.8	556	1	OCN3_HUMAN	Q75751 homo sapien
2	696.5	24.4	551	1	OCN3_MOUSE	Q9wtw5 mus musculu
3	696.5	24.4	551	1	OCN3_RAT	Q88446 rattus norv
4	641	22.5	557	1	OCN2_HUMAN	Q76082 homo sapien
5	639.5	22.4	557	1	OCN2_MOUSE	Q9z0e8 mus musculu
6	630.5	22.1	557	1	OCN2_RAT	Q70594 rattus norv
7	400.5	14.1	464	1	YT13_CAEEL	Q10917 caenorhabdi
8	387	13.6	529	1	YOU1_CAEEL	P30638 caenorhabdi
9	352.5	12.4	516	1	BOCT_RAT	Q9p290 rattus norv

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	2849	100.0	550	4	Q8N192	Q8n192 homo sapien
2	2832.5	99.4	563	4	O95742	O95742 homo sapien
3	2600	91.3	506	4	Q9NQC2	Q9nqc2 homo sapien
4	2583.5	90.7	519	4	Q9NQA6	Q9nqa6 homo sapien
5	2571.5	90.3	551	6	Q9TSY7	Q9tsy7 oryctolagus
6	2549.5	89.5	551	11	Q35956	Q35956 ratus norv
7	2524.5	88.6	547	6	Q8MK48	Q8mk48 sus scrofa
8	2463.5	86.5	545	11	Q8VC69	Q8vc69 mus musculu
9	2449.5	86.0	545	11	Q61185	Q61185 mus musculu
10	2437.5	85.6	533	6	Q8MK47	Q8mk47 sus scrofa
11	1421	49.9	542	6	Q8HY24	Q8hy24 oryctolagus
12	1416	49.7	542	4	Q8TCC7	Q8tcc7 homo sapien

#### RESULT 2

O95742

ID O95742 PRELIMINARY; PRT; 563 AA.  
AC O95742; O95187; Q9UEQ8; Q9UBG6;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Renal organic anion transport protein 1.  
GN SLC22A6 OR OAT1 OR ROAT1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=KIDNEY;  
RX MEDLINE=99103997; PubMed=9887087;  
RA Hosoyamada M., Sekine T., Kanai Y., Endou H.;  
RT "Molecular cloning and functional expression of a multispecific  
RT organic anion transporter from human kidney.";  
RL Am. J. Physiol. 276:F122-F128(1999).  
RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98433806; PubMed=9762842;  
 RA Reid G., Wolff N.A., Dautzenberg F.M., Burckhardt G.;  
 RT "Cloning of a human renal p-aminohippurate transporter, hOAT1.";  
 RL Kidney Blood Press. Res. 21:233-237(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=99137667; PubMed=9950961;  
 RA Lu R., Chan B.S., Schuster V.L.;  
 RT "Cloning of the human kidney PAH transporter: narrow substrate specificity and regulation by protein kinase C.";  
 RL Am. J. Physiol. 276:F295-F303(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=99160894; PubMed=10049739;  
 RA Race J.E., Grassl S.M., Williams W.J., Holtzman E.J.;  
 RT "Molecular cloning and characterization of two novel human renal organic anion transporters (hOAT1 and hOAT3)." ;  
 RL Biochem. Biophys. Res. Commun. 255:508-514(1999).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=99393620; PubMed=10462545;  
 RA Cihlar T., Lin D.C., Pritchard J.B., Fuller M.D., Mendel D.B.,  
 RA Sweet D.H.;  
 RT "The antiviral nucleotide analogs cidofovir and adefovir are novel substrates for human and rat renal organic anion transporter 1.";  
 RL Mol. Pharmacol. 56:570-580(1999)..  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Bahn A., Prawitt D., Reid G., Enklaar T., Wolff N.A., Hillemann A.,  
 RA Godehardt S., Buttler D., Knabe M., Schulten H.J., Gunawan B.,  
 RA Fuezesi L., Zabel B., Burckhardt G.;  
 RT "Genomic cloning and characterization of the human renal organic anion transporter gene (hOAT1)." ;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: MEDIATES THE NA(+) -INDEPENDENT TRANSPORT OF ORGANIC ANIONS SUCH AS P-AMINOHIPPURATE AND ALPHA-KETOGLUTARATE.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL MEMBRANE (POTENTIAL).  
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HOAT1-1 (SHOWN HERE) AND HOAT1-2; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY. ALSO DETECTED IN BRAIN AND AT LOW LEVELS, IN SKELETAL MUSCLE AND PLACENTA. NOT EXPRESSED IN HEART, LUNG, LIVER, PANCREAS, COLON, THYMUS, SMALL INTESTINE OR PERIPHERAL BLOOD LEUKOCYTES. IN THE KIDNEY, STRONGLY EXPRESSED IN PROXIMAL TUBULE CELLS.  
 CC -!- PTM: GLYCOSYLATED.  
 CC -!- SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS.  
 DR EMBL; AF057039; AAC70004.1; -.  
 DR EMBL; AB009697; BAA75072.1; -.  
 DR EMBL; AF104038; AAD10052.1; -.  
 DR EMBL; AB009698; BAA75073.1; -.  
 DR EMBL; AF097490; AAD19356.1; -.  
 DR EMBL; AF124373; AAD55356.1; -.  
 DR EMBL; AJ249369; CAB77184.1; -.  
 DR Genew; HGNC:10970; SLC22A6.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR004749; Orgcat\_transp.  
 DR InterPro; IPR005828; Sub\_transporter.  
 DR Pfam; PF00083; sugar\_tr; 1.  
 DR TIGRFAMs; TIGR00898; 2A0119; 1.  
 DR PROSITE; PS50850; MFS; 1.  
 KW Transmembrane; Transport; Alternative splicing; Ion transport;  
 KW Glycoprotein.  
 FT TRANSMEM 136 156 POTENTIAL.  
 FT TRANSMEM 185 205 POTENTIAL.  
 FT TRANSMEM 249 269 POTENTIAL.  
 FT TRANSMEM 338 358 POTENTIAL.

FT	TRANSMEM	396	416	POTENTIAL.
FT	TRANSMEM	426	446	POTENTIAL.
FT	TRANSMEM	485	505	POTENTIAL.
FT	CARBOHYD	39	39	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	56	56	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	92	92	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	97	97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	113	113	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	523	535	MISSING (IN ISOFORM HOAT1-2).
FT	CONFLICT	14	14	G -> S (IN REF. 3).
FT	CONFLICT	563	563	L -> F (IN REF. 2).
SQ	SEQUENCE	563 AA;	61816 MW;	74AD3EA2678032E4 CRC64;

Query Match 99.4%; Score 2832.5; DB 4; Length 563;  
 Best Local Similarity 97.7%; Pred. No. 4.4e-227;  
 Matches 550; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy	1 MAFNDLLQQVGGVGRFQQIQVTLVLPPLLMAHNTLQNFTAAIPTHCRPPADANLSKN	60
Db	1 MAFNDLLQQVGGVGRFQQIQVTLVLPPLLMAHNTLQNFTAAIPTHCRPPADANLSKN	60
Qy	61 GGLEVWLPRDRQGPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI	120
Db	61 GGLEVWLPRDRQGPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI	120
Qy	121 VTEWDLVCSSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA	180
Db	121 VTEWDLVCSSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA	180
Qy	181 FAPNFPPIYCAFRLLSGMALAGISLNCTLNVEWMPHIHTRACVGTLIGYVYSLGQFLLAGV	240
Db	181 FAPNFPPIYCAFRLLSGMALAGISLNCTLNVEWMPHIHTRACVGTLIGYVYSLGQFLLAGV	240
Qy	241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE	300
Db	241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE	300
Qy	301 GAKLSMEVLRASLQKELTMGKQASAMELLRCPTLRHFLCLSMWFATSFAYYGLVMDL	360
Db	301 GAKLSMEVLRASLQKELTMGKQASAMELLRCPTLRHFLCLSMWFATSFAYYGLVMDL	360
Qy	361 QGFGVSIYLIQVIFGAVDLPKA LGFLVINS LGRRPAQMAALLLAGICILLNGVIPQDQS	420
Db	361 QGFGVSIYLIQVIFGAVDLPKA LGFLVINS LGRRPAQMAALLLAGICILLNGVIPQDQS	420
Qy	421 IVRTSLAVLGKGCLAASFNCIFLYTGE LYPTMIRQTGMGMGSTMARVGSIVSPLVSM TAE	480
Db	421 IVRTSLAVLGKGCLAASFNCIFLYTGE LYPTMIRQTGMGMGSTMARVGSIVSPLVSM TAE	480
Qy	481 LYPSMPLFIYGA VPVAASAVTLLP ETLGQPLPDTVQDLES-----RKGKQT	527
Db	481 LYPSMPLFIYGA VPVAASAVTLLP ETLGQPLPDTVQDLES RWAPTQEAGIYPRKGKQT	540
Qy	528 RQQQEHQKYMVPLQASAQEKNGL	550
Db	541 RQQQEHQKYMVPLQASAQEKNGL	563

#### RESULT 6

035956

ID 035956 PRELIMINARY; PRT; 551 AA.  
 AC 035956;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Renal organic anion transport protein 1.  
 GN SLC22A6 OR ROAT1.  
 OS *Rattus norvegicus* (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=98043701; PubMed=9374486;  
 RA Sweet D.H., Wolff N.A., Pritchard J.B.;  
 RT "Expression cloning and characterization of ROAT1. The basolateral  
 organic anion transporter in rat kidney.";  
 RL J. Biol. Chem. 272:30088-30095(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;  
 RX MEDLINE=97373539; PubMed=9228014;  
 RA Sekine T., Watanabe N., Hosoyamada M., Kanai Y., Endou H.;  
 RT "Expression cloning and characterization of a novel multispecific  
 organic anion transporter.";  
 RL J. Biol. Chem. 272:18526-18529(1997).  
 CC -!- FUNCTION: MEDIATES THE NA(+) -INDEPENDENT TRANSPORT OF ORGANIC  
 CC ANIONS SUCH AS CYCLIC NUCLEOTIDES, PROSTAGLANDIN E2 AND URIC ACID.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL  
 CC MEMBRANE (POTENTIAL).  
 CC -!- TISSUE SPECIFICITY: STRONG EXPRESSION IN KIDNEY. VERY WEAK  
 CC EXPRESSION IN BRAIN. NOT DETECTED IN HEART, LUNG, LIVER, SPLEEN  
 CC SKELETAL MUSCLE, SMALL INTESTINE, LARGE INTESTINE, EYE OR TESTIS.  
 CC EXPRESSED IN THE PROXIMAL TUBULE IN THE KIDNEY.  
 CC -!- PTM: GLYCOSYLATED (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS.  
 DR EMBL; AF008221; AAC18772.1; -.  
 DR EMBL; AB004559; BAA22086.1; -.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR004749; Orgcat\_transp.  
 DR InterPro; IPR005828; Sub\_transporter.  
 DR Pfam; PF00083; sugar\_tr; 1.  
 DR TIGRFAMs; TIGR00898; 2A0119; 1.  
 DR PROSITE; PS50850; MFS; 1.  
 KW Transmembrane; Transport; Glycoprotein; Ion transport.  
 FT TRANSMEM 136 156 POTENTIAL.  
 FT TRANSMEM 196 216 POTENTIAL.  
 FT TRANSMEM 249 269 POTENTIAL.  
 FT TRANSMEM 338 358 POTENTIAL.  
 FT TRANSMEM 396 416 POTENTIAL.  
 FT TRANSMEM 485 505 POTENTIAL.  
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 551 AA; 60766 MW; 8BA47BEG28324BF2 CRC64;

Query Match 89.5%; Score 2549.5; DB 11; Length 551;  
Best Local Similarity 87.8%; Pred. No. 1.5e-203;  
Matches 484; Conservative 35; Mismatches 31; Indels 1; Gaps 1;

Qy	1	MAFNNDLLQQVGGVGRFQQIQVTLVVLPLLMASHNTLQNFTAAIPTHCRPPADANLSKN	60
:     :     :   :   :     :     :     :     :   :   :			
Db	1	MAFNNDLLKQVGGVGRFQLIQVTMVVAPLLMASHNTLQNFTAAIPPHCRPPANANLSKD	60
:   :     :   :   :     :     :     :   :   :			
Qy	61	GGLEVWLPRDRQGQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI	120
:   :     :   :   :     :     :     :   :   :			
Db	61	GGLEAWLPLDKQGQPESCLRFTSPQWGPPFYNGTEANGTRVTEPCIDGWVYDNSTFPSTI	120
:   :     :   :   :     :     :     :   :   :			
Qy	121	VTEWDLVCSHRALRQLAQSLYMGVVLGAMVFGYLADRLGRRKVILINYLQTAVGSGTCAA	180
:         :     :     :     :     :     :     :     :   :			
Db	121	VTEWNLVCSHRAFRQLAQSLYMGVVLGAMVFGYLADRLGRRKVILINYLQTAVGSGTCAA	180
:   :     :   :   :     :     :     :   :   :			
Qy	181	FAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPITHTRACVGTЛИGVYSLGQFLLAGV	240
:    : :   :     :   :   :     :     :     :   :   :			
Db	181	YAPNYTVYCVFRLLSGMSLASIAINCMTLNVEWMPITHRAYVGTЛИGVYSLGQFLLAGI	240
:   :     :   :   :     :     :     :   :   :			

QY 241 AYAVPHWRHLQLLVSAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 241 AYAVPHWRHLQLVVSPFFIAFIYSWFFIESARWYSSSGRLDLTLRALQRVARINGQEE 300  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 301 GAKLSMEVLRASLQKELTMGKQASAMELLRCPTLRLFLCLSMWFATSFAYYGLVMDL 360  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 301 GAKLSIEVLRTSLQKELTLSKGQASAMELLRCPTLRLFLCLSMWFATSFAYYGLVMDL 360  
 |||||:|||||:|||||:|||||:|||||:|||||:  
 QY 361 QGFGVSIYLIQVIFGAVIDPAKLVGFLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 361 QGFGVSMYLIQVIFGAVIDPAKFVCFLVINSMGRPAQMASLLLACICILVNGIIPKSHT 420  
 |||||:|||||:|||||:|||||:  
 QY 421 IIRTSALVLGKGCLAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480  
 |||||:|||||:|||||:|||||:|||||:|||||:  
 Db 421 IIRTSALVLGKGCLASSFNCIFLYTGELEYPTVIRQTGLGMGSTMARVGSIVSPLVSMTAE 480  
 |||||:|||||:  
 Qy 481 LYPSMPLFIYGAAPVAASAVTVLLPETLGQPLPDTVQDLESR-KGKQTRQQQEHQKYMVP 539  
 |||||:|||||:|||||:|||||:|||||:|||||:  
 Db 481 FYPSTMPLFIYGAAPVVASAVTALLPETLGQPLPDTVQDLKSRSGKQNQQQQEQQQKQMMMP 540  
 |||||:  
 Qy 540 LQASAQEKNGL 550  
 |||||:  
 Db 541 LQASTQEKNGL 551

RESULT 9

Q61185

ID Q61185 PRELIMINARY; PRT; 545 AA.  
 AC Q61185;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Kidney-specific transport protein.  
 GN SLC22A6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=97197822; PubMed=9045672;  
 RA Lopez-Nieto C.E., You G., Bush K.T., Barros E.J., Beier D.R.,  
 RA Nigam S.K.;  
 RT "Molecular cloning and characterization of NKT, a gene product related  
 to the organic cation transporter family that is almost exclusively  
 expressed in the kidney.";  
 RL J. Biol. Chem. 272:6471-6478 (1997).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 DR EMBL; U52842; AAC53112.1; -.  
 DR MGD; MGI:892001; Slc22a6.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR004749; Orgcat\_transp.  
 DR InterPro; IPR005828; Sub\_transporter.  
 DR Pfam; PF00083; sugar\_tr; 1.  
 DR TIGRFAMs; TIGR00898; 2A0119; 1.  
 DR PROSITE; PS50850; MFS; 1.  
 KW Transmembrane.  
 SQ SEQUENCE 545 AA; 59983 MW; CD3B762E5984933A CRC64;

Query Match 86.0%; Score 2449.5; DB 11; Length 545;  
 Best Local Similarity 84.9%; Pred. No. 3e-195;  
 Matches 468; Conservative 41; Mismatches 35; Indels 7; Gaps 2;

QY 1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLASHNTLQNFTAAIPTHHCRPPADANLSKN 60  
 |||||:|||||:|||||:|||||:  
 Db 1 MAFNDLLKQVGGVGRFQLIQVTMVVAPLLLASHNTLQNFTAAIPAHHCRPPANANLSKD 60  
 |||||:  
 QY 61 GGLEVWLPRDRQGPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120  
 |||||:|||||:  
 Db 61 GGLEARLPLDKQGRPESCLRFPFPH-----NGTEANGTGVTEPCLDGWVYDNSTFPSTI 114

Qy	121 VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA	180
	:       :       :       :       :       :       :       :       :	
Db	115 VTEWNLVCSHRAFRQLAQSLFMVGVLLGAMMFGYLADRLGRRKVLILNYLQTAVSGTCAA	174
Qy	181 FAPNFPIYCAFRLLSGMALAGISLNCTLNVEWMPHIHTRACVGTLLIGYVYSLGQFLLAGV	240
	:     : :     :     :     :     :     :     :     :     :     :     :     :	
Db	175 YAPNYTVYCIFRLLSGMSLASIAINCMTLNMEWMPHIHTRAYVGTLLIGYVYSLGQFLLAGI	234
Qy	241 AYAVPHWRHLQLLVASAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE	300
	:       :       :       :       :       :       :       :       :	
Db	235 AYAVPHWRHLQLAVSVPFFVAIFIYSWFFIESARWYSSSGRLDLTLRALQRVARINGKQEE	294
Qy	301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWFATSFAYYGLVMDL	360
	:     :       :       :       :       :       :       :       :	
Db	295 GAKLSIEVLQTSLQKELTLNKGQASAMELLRCPTLRRFLCLSMWFATSFAYYGLVMDL	354
Qy	361 QGFGVSIYLIQVIFGAVDLPAKLVGFLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS	420
	:       :       :       :       :       :       :       :       :     :	
Db	355 QGFGVSMYLIQVIFGAVDLPAKFVCFLVINSMGRRPAQLASLLLALGICILVNGIIPRGHT	414
Qy	421 IVRTSLAVLGKGCLAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE	480
	:       :       :       :       :       :       :       :       :       :	
Db	415 IIRTSLAVLGKGCLASSFNCIFLYTGELEYPTMIRQTGLGMGSTMARVGSIVSPLISMATAE	474
Qy	481 LYPSPMLFIYGVPAVASAVTULLPETLGQPLPDTVQDLESR-KGKQTRQQQEHQKYMVP	539
	:       :       :       :       :       :     :     :     :     :     :	
Db	475 FYPSIPLFIFGAVPVAAASAVTALLPETLGQPLPDTVQDLKSRSRGKQKQQQLEQQKQMIP	534
Qy	540 LQASAQEKNGL	550
	:	
Db	535 LQVSTQEKNGL	545

Sekine T et al., Expression cloning and characterization of a novel multispecific organic anion transporter. J Biol Chem. 1997 Jul 25;272(30):18526-9.